

SEQUENCE LISTING

<110> Ajinomoto Co. Inc.

<120> Method for Producing L-Amino Acid Using Methylotroph

<130> OP1629

<150> JP 2002-336346

<151> 2002-11-20

<160> 14

<170> PatentIn Ver. 2.0

<210> 1

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 1

aggaaattcc ccgttctgga taatgtttt tgcgccgac

39

<210> 2

<211> 58

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 2

cggatgcatac tagagttaac ctgcagggtg aaattgttat ccgctcacaa ttccacac 58

<210> 3
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 3
tgacctgcag gtttgcacag aggatggccc atgtt 35

<210> 4
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 4
cattcttagat cccttaaactt tacagcaaac cgccat 36

<210> 5
<211> 64
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 5
catttcctgc aggcaaagga gatgagcgta atggatca tggaaatctt cattacaggt 60
ctgc 64

<210> 6
<211> 50
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 6

ggcgagcta gaagagctcc aaaacccgcg aaaactaacc catcaacatc 50

<210> 7

<211> 711

<212> DNA

<213> Brevibacterium lactofermentum

<220>

<221> CDS

<222> (1)..(711)

<400> 7

atg gtg atc atg gaa atc ttc att aca ggt ctg ctt ttg ggg gcc agt 48
Met Val Ile Met Glu Ile Phe Ile Thr Gly Leu Leu Leu Gly Ala Ser
1 5 10 15

ctt tta ctg tcc atc gga ccg cag aat gta ctg gtg att aaa caa gga 96
Leu Leu Leu Ser Ile Gly Pro Gln Asn Val Leu Val Ile Lys Gln Gly
20 25 30

att aag cgc gaa gga ctc att gcg gtt ctt ctc gtg tgt tta att tct 144
Ile Lys Arg Glu Gly Leu Ile Ala Val Leu Leu Val Cys Leu Ile Ser
35 40 45

gac gtc ttt ttg ttc atc gcc ggc acc ttg ggc gtt gat ctt ttg tcc 192
Asp Val Phe Leu Phe Ile Ala Gly Thr Leu Gly Val Asp Leu Leu Ser
50 55 60

aat gcc gcg ccg atc gtg ctc gat att atg cgc tgg ggt ggc atc gct 240
Asn Ala Ala Pro Ile Val Leu Asp Ile Met Arg Trp Gly Gly Ile Ala
65 70 75 80

tac ctg tta tgg ttt gcc gtc atg gca gcg aaa gac gcc atg aca aac 288
Tyr Leu Leu Trp Phe Ala Val Met Ala Ala Lys Asp Ala Met Thr Asn
85 90 95

aag gtg gaa gcg cca cag atc att gaa gaa aca gaa cca acc gtg ccc 336

Lys	Val	Glu	Ala	Pro	Gln	Ile	Ile	Glu	Glu	Thr	Glu	Pro	Thr	Val	Pro	
				100				105			110					
gat	gac	acg	cct	ttg	ggc	ggt	tgc	gcg	gtg	gcc	act	gac	acg	cgc	aac	384
Asp	Asp	Thr	Pro	Ieu	Gly	Gly	Ser	Ala	Val	Ala	Thr	Asp	Thr	Arg	Asn	
				115				120			125					
cgg	gtg	cgg	gtg	gag	gtg	agc	gtc	gat	aag	cag	cgg	gtt	tgg	gta	aag	432
Arg	Val	Arg	Val	Glu	Val	Ser	Val	Asp	Lys	Gln	Arg	Val	Trp	Val	Lys	
				130				135			140					
ccc	atg	ttg	atg	gca	atc	gtg	ctg	acc	tgg	ttg	aac	ccg	aat	gcg	tat	480
Pro	Met	Leu	Met	Ala	Ile	Val	Leu	Thr	Trp	Leu	Asn	Pro	Asn	Ala	Tyr	
				145				150			155			160		
ttg	gac	gcg	ttt	gtg	ttt	atc	ggc	ggc	gtc	ggc	gca	caa	tac	ggc	gac	528
Leu	Asp	Ala	Phe	Val	Phe	Ile	Gly	Gly	Val	Gly	Ala	Gln	Tyr	Gly	Asp	
				165				170			175					
acc	gga	cgg	tgg	att	ttc	gcc	gct	ggc	gcf	ttc	gcf	gca	agc	ctg	atc	576
Thr	Gly	Arg	Trp	Ile	Phe	Ala	Ala	Gly	Ala	Phe	Ala	Ala	Ser	Leu	Ile	
				180				185			190					
tgg	ttc	ccg	ctg	gtg	ggt	ttc	ggc	gca	gca	gca	ttg	tca	cgc	ccg	ctg	624
Trp	Phe	Pro	Leu	Val	Gly	Phe	Gly	Ala	Ala	Ala	Leu	Ser	Arg	Pro	Leu	
				195				200			205					
tcc	agc	ccc	aag	gtg	tgg	cgc	tgg	atc	aac	gtc	gtc	gtg	gca	gtt	gtg	672
Ser	Ser	Pro	Lys	Val	Trp	Arg	Trp	Ile	Asn	Val	Val	Val	Ala	Val	Val	
				210				215			220					
atg	acc	gca	ttg	gcc	atc	aaa	ctg	atg	ttg	atg	ggt	tag				711
Met	Thr	Ala	Leu	Ala	Ile	Lys	Leu	Met	Leu	Met	Gly					
				225				230.			235					

<210> 8

<211> 236

<212> PRT

<213> *Brevibacterium lactofermentum*

<400> 8

Met Val Ile Met Glu Ile Phe Ile Thr Gly Leu Leu Leu Gly Ala Ser

1 5 10 15

Leu Leu Leu Ser Ile Gly Pro Gln Asn Val Leu Val Ile Lys Gln Gly

20	25	30
Ile Lys Arg Glu Gly Leu Ile Ala Val Leu Leu Val Cys Leu Ile Ser		
35	40	45
Asp Val Phe Leu Phe Ile Ala Gly Thr Leu Gly Val Asp Leu Leu Ser		
50	55	60
Asn Ala Ala Pro Ile Val Leu Asp Ile Met Arg Trp Gly Gly Ile Ala		
65	70	75
Tyr Leu Leu Trp Phe Ala Val Met Ala Ala Lys Asp Ala Met Thr Asn		
85	90	95
Lys Val Glu Ala Pro Gln Ile Ile Glu Glu Thr Glu Pro Thr Val Pro		
100	105	110
Asp Asp Thr Pro Leu Gly Gly Ser Ala Val Ala Thr Asp Thr Arg Asn		
115	120	125
Arg Val Arg Val Glu Val Ser Val Asp Lys Gln Arg Val Trp Val Lys		
130	135	140
Pro Met Leu Met Ala Ile Val Leu Thr Trp Leu Asn Pro Asn Ala Tyr		
145	150	155
160		
Leu Asp Ala Phe Val Phe Ile Gly Gly Val Gly Ala Gln Tyr Gly Asp		
165	170	175
Thr Gly Arg Trp Ile Phe Ala Ala Gly Ala Phe Ala Ala Ser Leu Ile		
180	185	190
Trp Phe Pro Leu Val Gly Phe Gly Ala Ala Ala Leu Ser Arg Pro Leu		
195	200	205
Ser Ser Pro Lys Val Trp Arg Trp Ile Asn Val Val Val Ala Val Val		
210	215	220
Met Thr Ala Leu Ala Ile Lys Leu Met Leu Met Gly		
225	230	235

<210> 9

<211> 712

<212> DNA

<213> *Brevibacterium lactofermentum*

<220>

<221> CDS

<222> (1)...(375)

<400> 9
 atg gtg atc atg gaa atc ttc att aca ggt ctg ctt ttg ggg gcc agt 48
 Met Val Ile Met Glu Ile Phe Ile Thr Gly Leu Leu Leu Gly Ala Ser
 1 5 10 15
 ctt ttg ctg tcc atc gga ccg cag aat gta ctg gtg att aaa caa gga 96
 Leu Leu Leu Ser Ile Gly Pro Gln Asn Val Leu Val Ile Lys Gln Gly
 20 25 30
 att aag cgc gaa gga ctc att gcg gtt ctt ctc gtg tgt tta att tct 144
 Ile Lys Arg Glu Gly Leu Ile Ala Val Leu Leu Val Cys Leu Ile Ser
 35 40 45
 gac gtc ttt ttg ttc atc gcc ggc acc ttg ggc gtt gat ctt ttg tcc 192
 Asp Val Phe Leu Phe Ile Ala Gly Thr Leu Gly Val Asp Leu Leu Ser
 50 55 60
 aat gcc gcg ccg atc gtg ctc gat att atg cgc tgg ggt ggc atc gct 240
 Asn Ala Ala Pro Ile Val Leu Asp Ile Met Arg Trp Gly Gly Ile Ala
 65 70 75 80
 tac ctg tta tgg ttt gcc gtc atg gca gcg aaa gac gcc atg aca aac 288
 Tyr Leu Leu Trp Phe Ala Val Met Ala Ala Lys Asp Ala Met Thr Asn
 85 90 95
 aag gtg gaa gcg cca cag atc att gaa gaa aca gaa cca acc gtg ccc 336
 Lys Val Glu Ala Pro Gln Ile Ile Glu Glu Thr Glu Pro Thr Val Pro
 100 105 110
 gat gac acg cct ttg ggc gtg ttc ggc ggt ggc cac tga cacgcgcac 385
 Asp Asp Thr Pro Leu Gly Val Phe Gly Gly His
 115 120 125
 cgggtgcggg tggaggtgag cgtcgataag cagcgggtt gggtaagcc catgttgatg 445
 gcaatcgtgc tgacctggtt gaaccgaaat gcgtatttgg acgcgtttgt gtttatcggc 505
 ggctcgcccg cgcaatacgg cgacaccgga cggtgattt tcgcccgtgg cgcttcgcg 565
 gcaaggctga tctggttccc gctggtggtt ttcggcgcag cagcattgtc acgcccgtg 625
 tccagccccca aggtgtggcg ctggatcaac gtcgtcgtgg cagttgtgat gaccgcattg 685
 gccatcaaac tgatgttgat ggtag 712

<210> 10

<211> 124

<212> PRT

<213> *Brevibacterium lactofermentum*

<400> 10

Met Val Ile Met Glu Ile Phe Ile Thr Gly Leu Leu Leu Gly Ala Ser
1 5 10 15
Leu Leu Leu Ser Ile Gly Pro Gln Asn Val Leu Val Ile Lys Gln Gly
20 25 30
Ile Lys Arg Glu Gly Leu Ile Ala Val Leu Leu Val Cys Leu Ile Ser
35 40 45
Asp Val Phe Leu Phe Ile Ala Gly Thr Leu Gly Val Asp Leu Leu Ser
50 55 60
Asn Ala Ala Pro Ile Val Leu Asp Ile Met Arg Trp Gly Gly Ile Ala
65 70 75 80
Tyr Leu Leu Trp Phe Ala Val Met Ala Ala Lys Asp Ala Met Thr Asn
85 90 95
Lys Val Glu Ala Pro Gln Ile Ile Glu Glu Thr Glu Pro Thr Val Pro
100 105 110
Asp Asp Thr Pro Leu Gly Val Phe Gly Gly His
115 120

<210> 11

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 11

ccccccggat ttccttcctc cggtctgctt 30

<210> 12

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 12
 taaagcttgg tcagggcggtt ggccgtggcg 30

<210> 13
 <211> 1197
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (272)..(1153)

<400> 13
 ccaggcgact gtcttcaata ttacagccgc aactactgac atgacgggtg atggtgttca 60
 caattccacg gcatcgca cccaacgcag tgatcaccag ataatgtgtt gcatgcacag 120
 tgctaaactg gttattcctt taaggggtga gttgttctta aggaaagcat aaaaaaaaaca 180
 tgcataacaac aatcagaacg gttctgtctg cttgctttta atgccataacc aaacgtacca 240
 ttgagacact tgtttgacaca gaggatggcc c atg ttc acg gga agt att gtc 292
 Met Phe Thr Gly Ser Ile Val
 1 5

gcg att gtt act ccg atg gat gaa aaa ggt aat gtc tgt cggt gct agc 340
 Ala Ile Val Thr Pro Met Asp Glu Lys Gly Asn Val Cys Arg Ala Ser
 10 15 20

ttg aaa aaa ctg att gat tat cat gtc gcc agc ggt act tcg cggt atc 388
 Leu Lys Leu Ile Asp Tyr His Val Ala Ser Gly Thr Ser Ala Ile
 25 30 35

gtt tct gtt ggc acc act ggc gag tcc gct acc tta aat cat gac gaa 436
 Val Ser Val Gly Thr Thr Gly Glu Ser Ala Thr Leu Asn His Asp Glu
 40 45 50 55

cat gct gat gtg gtg atg atg acg ctg gat ctg gct gat ggg cggt att 484
 His Ala Asp Val Val Met Met Thr Leu Asp Leu Ala Asp Gly Arg Ile
 60 65 70

ccg gta att gcc ggg acc ggc gct aac gct act gcg gaa gcc att agc 532
 Pro Val Ile Ala Gly Thr Gly Ala Asn Ala Thr Ala Glu Ala Ile Ser
 75 80 85

ctg acg cag cgc ttc aat gac agt ggt atc gtc ggc tgc ctg acg gta 580

Leu	Thr	Gln	Arg	Phe	Asn	Asp	Ser	Gly	Ile	Val	Gly	Cys	Leu	Thr	Val	
90									95					100		
acc	cct	tac	tac	aat	cgt	ccg	tcg	caa	gaa	ggt	ttg	tat	cag	cat	ttc	628
Thr	Pro	Tyr	Tyr	Asn	Arg	Pro	Ser	Gln	Glu	Gly	Leu	Tyr	Gln	His	Phe	
105									110				115			
aaa	gcc	atc	gct	gag	cat	act	gac	ctg	ccg	caa	att	ctg	tat	aat	gtg	676
Lys	Ala	Ile	Ala	Glu	His	Thr	Asp	Leu	Pro	Gln	Ile	Leu	Tyr	Asn	Val	
120									125			130		135		
ccg	tcc	cgt	act	ggc	tgc	gat	ctg	ctc	ccg	gaa	acg	gtg	ggc	cgt	ctg	724
Pro	Ser	Arg	Thr	Gly	Cys	Asp	Leu	Leu	Pro	Glu	Thr	Val	Gly	Arg	Leu	
140									145			150				
gcg	aaa	gta	aaa	aat	att	atc	gga	atc	aaa	gag	gca	aca	ggg	aac	tta	772
Ala	Lys	Val	Lys	Asn	Ile	Ile	Gly	Ile	Lys	Glu	Ala	Thr	Gly	Asn	Leu	
155									160			165				
acg	cgt	gta	aac	cag	atc	aaa	gag	ctg	gtt	tca	gat	gat	ttt	gtt	ctg	820
Thr	Arg	Val	Asn	Gln	Ile	Lys	Glu	Leu	Val	Ser	Asp	Asp	Phe	Val	Leu	
170									175			180				
ctg	agc	ggc	gat	gat	gct	agc	gct	gac	ttc	atg	caa	ttg	ggc	ggt		868
Leu	Ser	Gly	Asp	Asp	Ala	Ser	Ala	Leu	Asp	Phe	Met	Gln	Ieu	Gly	Gly	
185									190			195				
cat	ggg	gtt	att	tcc	gtt	acg	act	aac	gtc	gca	gct	cgt	gat	atg	gcc	916
His	Gly	Val	Ile	Ser	Val	Thr	Thr	Asn	Val	Ala	Ala	Arg	Asp	Met	Ala	
200									205			210		215		
cag	atg	tgc	aaa	ctg	gca	gca	gaa	gaa	cat	ttt	gcc	gag	gca	cgc	gtt	964
Gln	Met	Cys	Lys	Ieu	Ala	Ala	Glu	Glu	His	Phe	Ala	Glu	Ala	Arg	Val	
220									225			230				
att	aat	cag	cgt	ctg	atg	cca	tta	cac	aac	aaa	cta	ttt	gtc	gaa	ccc	1012
Ile	Asn	Gln	Arg	Leu	Met	Pro	Leu	His	Asn	Lys	Ieu	Phe	Val	Glu	Pro	
235									240			245				
aat	cca	atc	ccg	gtg	aaa	tgg	gca	tgt	aag	gaa	ctg	ggt	ctt	gtg	gct	1060
Asn	Pro	Ile	Pro	Val	Lys	Trp	Ala	Cys	Lys	Glu	Ieu	Gly	Ieu	Val	Ala	
250									255			260				
acc	gat	acg	ctg	cgc	ctg	cca	atg	aca	cca	atc	acc	gac	agt	ggt	cgt	1108
Thr	Asp	Thr	Leu	Arg	Leu	Pro	Met	Thr	Pro	Ile	Thr	Asp	Ser	Gly	Arg	
265									270			275				
gag	acg	gtc	aga	gct	gct	ctt	aag	cat	gcc	ggt	ttg	ctg	taa			1150
Glu	Thr	Val	Arg	Ala	Ala	Leu	Lys	His	Ala	Gly	Ieu	Ieu				

280	285	290	
agtttaggga	gatttgatgg	cttactctgt	tcaaaaagtcg
			cgcctgg
			1197
<210> 14			
<211> 292			
<212> PRT			
<213> Escherichia coli			
<400> 14			
Met Phe Thr Gly Ser Ile Val Ala Ile Val Thr Pro Met Asp Glu Lys			
1	5	10	15
Gly Asn Val Cys Arg Ala Ser Leu Lys Lys Leu Ile Asp Tyr His Val			
20	25	30	
Ala Ser Gly Thr Ser Ala Ile Val Ser Val Gly Thr Thr Gly Glu Ser			
35	40	45	
Ala Thr Leu Asn His Asp Glu His Ala Asp Val Val Met Met Thr Leu			
50	55	60	
Asp Leu Ala Asp Gly Arg Ile Pro Val Ile Ala Gly Thr Gly Ala Asn			
65	70	75	80
Ala Thr Ala Glu Ala Ile Ser Leu Thr Gln Arg Phe Asn Asp Ser Gly			
85	90	95	
Ile Val Gly Cys Leu Thr Val Thr Pro Tyr Tyr Asn Arg Pro Ser Gln			
100	105	110	
Glu Gly Leu Tyr Gln His Phe Lys Ala Ile Ala Glu His Thr Asp Leu			
115	120	125	
Pro Gln Ile Leu Tyr Asn Val Pro Ser Arg Thr Gly Cys Asp Leu Leu			
130	135	140	
Pro Glu Thr Val Gly Arg Leu Ala Lys Val Lys Asn Ile Ile Gly Ile			
145	150	155	160
Lys Glu Ala Thr Gly Asn Leu Thr Arg Val Asn Gln Ile Lys Glu Leu			
165	170	175	
Val Ser Asp Asp Phe Val Leu Leu Ser Gly Asp Asp Ala Ser Ala Leu			
180	185	190	
Asp Phe Met Gln Leu Gly Gly His Gly Val Ile Ser Val Thr Thr Asn			
195	200	205	
Val Ala Ala Arg Asp Met Ala Gln Met Cys Lys Leu Ala Ala Glu Glu			
210	215	220	

His Phe Ala Glu Ala Arg Val Ile Asn Gln Arg Leu Met Pro Leu His
225 230 235 240
Asn Lys Leu Phe Val Glu Pro Asn Pro Ile Pro Val Lys Trp Ala Cys
 245 250 255
Lys Glu Leu Gly Leu Val Ala Thr Asp Thr Leu Arg Leu Pro Met Thr
 260 265 270
Pro Ile Thr Asp Ser Gly Arg Glu Thr Val Arg Ala Ala Leu Lys His
 275 280 285
Ala Gly Leu Leu
 290